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<150> UK 0317656.7
<151> 2003-07-28

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<170> PatentIn version 3.2

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atcgaggttt atttattaat ttgaatagat attaagtttt attatattta cacttacata  13800

ctaataataa attcaacaaa caatttattt atgtttattt atttattaaa aaaaaacaaa  13860

aactcaaaat ttcttctata aagtaacaaa acttttaaac attctctctt ttacaaaaat  13920

aaacttattt tgtactttaa aaacagtcat gttgtattat aaaataagta attagcttaa  13980

cttatacata atagaaacaa attatactta ttagtcagtc agaaacaact ttggcacata  14040

tcaatattat gctctcgaca aataactttt ttgcattttt tgcacgatgc atttgccttt  14100

cgccttattt tagaggggca gtaagtacag taagtacgtt ttttcattac tggctcttca  14160

gtactgtcat ctgatgtacc aggcacttca tttggcaaaa tattagagat attatcgcgc  14220

aaatatctct tcaaagtagg agcttctaaa cgcttacgca taaacgatga cgtcaggctc  14280
```

64

```
atgtaaaggt ttctcataaa ttttttgcga ctttggacct tttctccctt gctactgaca   14340

ttatggctgt atataataaa agaatttatg caggcaatgt ttatcattcc gtacaataat   14400

gccataggcc acctattcgt cttcctactg caggtcatca cagaacacat ttggtctagc   14460

gtgtccactc cgcctttagt ttgattataa tacataacca tttgcggttt accggtactt   14520

tcgttgatag aagcatcctc atcacaagat gataataagt ataccatctt agctggcttc   14580

ggtttatatg agacgagagt aaggggtccg tcaaaacaaa acatcgatgt tcccactggc   14640

ctggagcgac tgtttttcag tacttccggt atctcgcgtt tgtttgatcg cacggttccc   14700

acaatggttg cggccagccc                                              14720
```

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<210>  25
<211>  23
<212>  DNA
<213>  Artificial

<220>
<223>  PCR Primer

<400>  25
catcgatgcc cagcattgag atg                                            23


<210>  26
<211>  34
<212>  DNA
<213>  Artificial

<220>
<223>  PCR Primer

<400>  26
caagcaaagt gaacacgtcg ctaagcgaaa gcta                                34


<210>  27
<211>  28
<212>  DNA
<213>  Artificial

<220>
<223>  PCR Primer

<400>  27
gccatccacg ctgttttgac ctccatag                                       28


<210>  28
<211>  27
<212>  DNA
<213>  Artificial

<220>
<223>  PCR Primer

<400>  28
gccaatacaa tgtaggctgc tctacac                                        27
```

```
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<211>  1005
<212>  DNA
<213>  Artificial

<220>
<223>  coding region of tTA from pUHD15-1

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ttgtattggc atgtaaaaaa taagcgggct ttgctcgacg ccttagccat tgagatgtta   180

gataggcacc atactcactt ttgccctttta gaaggggaaa gctggcaaga ttttttacgt   ·240

aataacgcta aaagttttag atgtgcttta ctaagtcatc gcgatggagc aaaagtacat   300

ttaggtacac ggcctacaga aaaacagtat gaaactctcg aaaatcaatt agcctttttta   360

tgccaacaag ttttttcact agagaatgca ttatatgcac tcagcgctgt ggggcatttt   420

actttaggtt gcgtattgga agatcaagag catcaagtcg ctaaagaaga aagggaaaca   480

cctactactg atagtatgcc gccattatta cgacaagcta tcgaattatt tgatcaccaa   540

ggtgcagagc cagccttctt attcggcctt gaattgatca tatgcggatt agaaaaacaa   600

cttaaatgtg aaagtgggtc cgcgtacagc cgcgcgcgta cgaaaaacaa ttacgggtct   660

accatcgagg gcctgctcga tctcccggac gacgacgccc ccgaagaggc ggggctggcg   720

gctccgcgcc tgtcctttct ccccgcggga cacacgcgca gactgtcgac ggcccccccg   780

accgatgtca gcctggggga cgagctccac ttagacggcg aggacgtggc gatggcgcat   840

gccgacgcgc tagacgattt cgatctggac atgttggggg acggggattc cccgggtccg   900

ggatttaccc ccaccgactc cgcccctac ggcgctctgg atatggccga cttcgagttt   960

gagcagatgt ttaccgatgc ccttggaatt gacgagtacg gtggg               1005
```

```
<210>  30
<211>  336
<212>  PRT
<213>  Artificial

<220>
<223>  tTA

<400>  30

Met Gly Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu
1               5                   10                  15


Leu Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala
            20                  25                  30


Gln Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn
        35                  40                  45
```

66

Lys Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His
    50   55   60

His Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu
65   70   75   80

Arg Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp
                85   90   95

Gly Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu
            100   105   110

Thr Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu
        115   120   125

Glu Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly
    130   135   140

Cys Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu
145   150   155   160

Thr Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu
            165   170   175

Leu Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu
            180   185   190

Leu Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
    195   200   205

Ala Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu
    210   215   220

Gly Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu
225   230   235   240

Ala Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu
            245   250   255

Ser Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
            260   265   270

Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
    275   280   285

Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
    290   295   300

Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
305   310   315   320

```
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
            325                 330                 335
```

<210> 31
<211> 1017
<212> DNA
<213> Artificial

<220>
<223> tTAV

<400> 31

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accctctact ggcacgtgaa gaataagcgg gcgctgctgg atgccctggc catcgagatg     180

ctcgaccgcc accacacgca tttttgcccg ttggaaggcg agtcctggca ggacttcctc     240

cgcaataacg ccaagtcgtt ccgctgcgct ctgctgtccc accgagacgg tgccaaagtc     300

catctcggca cgcgcccgac cgaaaagcaa tacgagacac tggagaacca gctcgcgttc     360

ctgtgccagc aaggcttcag cctggaaaat gctctctacg ctctgagcgc cgtcggtcac     420

tttaccctgg gctgcgtgct ggaggaccaa gagcatcaag tcgcaaaaga ggagcgcgag     480

acccccaacaa ccgattcgat gcccccactg ctgcgtcagg caatcgagct gttcgatcat     540

caaggagccg agccggcatt cctgttcggc ttggagctga ttatctgcgg attggaaaag     600

caactgaaat gcgagtcggg ctcgggcccc gcgtacagcc gcgcgcgtac gaaaaacaat     660

tacgggtcta ccatcgaggg cctgctcgat ctcccggacg acgacgcccc cgaagaggcg     720

gggctggcgg ctccgcgcct gtcctttctc ccgcgcggac acacgcgcag actgtcgacg     780

gccccccga ccgatgtcag cctgggggac gagctccact tagacggcga ggacgtggcg     840

atggcgcatg ccgacgcgct agacgatttc gatctggaca tgttggggga cggggattcc     900

ccgggtccgg gatttacccc ccacgactcc gcccctacg gcgctctgga tatggccgac     960

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```

<210> 32
<211> 338
<212> PRT
<213> Artificial

<220>
<223> tTAV

<400> 32

```
Met Gly Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu
1               5                   10                  15


Leu Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala
            20                  25                  30
```

68

```
Gln Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn
         35              40              45
```

```
Lys Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His
         50              55              60
```

```
His Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu
65              70              75              80
```

```
Arg Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp
             85              90              95
```

```
Gly Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu
         100             105             110
```

```
Thr Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu
         115             120             125
```

```
Glu Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly
    130             135             140
```

```
Cys Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu
145             150             155             160
```

```
Thr Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu
             165             170             175
```

```
Leu Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu
             180             185             190
```

```
Leu Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
         195             200             205
```

```
Gly Pro Ala Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr
    210             215             220
```

```
Ile Glu Gly Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala
225             230             235             240
```

```
Gly Leu Ala Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg
             245             250             255
```

```
Arg Leu Ser Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu
         260             265             270
```

```
His Leu Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp
         275             280             285
```

69

```
Asp Phe Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly
    290             295             300
```

```
Phe Thr Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp
305             310             315             320
```

```
Phe Glu Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr
            325             330             335
```

```
Gly Gly
```

<210> 33
<211> 4455
<212> DNA
<213> Artificial

<220>
<223> pUHD15-1

<400> 33
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tcaattacgg ggtcattagt tcatagccca tatatggagt tccgcgttac ataacttacg       180

gtaaatggcc cgcctggctg accgcccaac gacccccgcc cattgacgtc aataatgacg       240

tatgttccca tagtaacgcc aatagggact ttccattgac gtcaatgggt ggagtattta       300

cgctaaactg cccacttggc agtacatcaa gtgtatcata tgccaagtac gccccctatt       360

gacgtcaatg acggtaaatg gcccgcctgg cattatgccc agtacatgac cttatgggac       420

tttcctactt ggcagtacat ctacgtatta gtcatcgcta ttaccatggt gatgcggttt       480

tggcagtaca tcaatgggcg tggatagcgg tttgactcac ggggatttcc aagtctccac       540

cccattgacg tcaatgggag tttgttttgg caccaaaatc aacgggactt tccaaaatgt       600

cgtaacaact ccgccccatt gacgcaaatg ggcggtaggc gtgtacggtg ggaggtctat       660

ataagcagag ctcgtttagt gaaccgtcag atcgcctgga cgccatcc acgctgtttt       720

gacctccata gaagacaccg ggaccgatcc agcctccgcg gccccgaatt catatgtcta       780

gattagataa aagtaaagtg attaacagcg cattagagct gcttaatgag gtcggaatcg       840

aaggtttaac aacccgtaaa ctcgcccaga agctaggtgt agagcagcct acattgtatt       900

ggcatgtaaa aaataagcgg gctttgctcg acgccttagc cattgagatg ttagataggc       960

accatactca cttttgccct ttagaagggg aaagctggca agattttttta cgtaataacg      1020

ctaaaagttt tagatgtgct ttactaagtc atcgcgatgg agcaaaagta catttaggta      1080

cacggcctac agaaaaacag tatgaaactc tcgaaaatca attagccttt ttatgccaac      1140

aaggtttttc actagagaat gcattatatg cactcagcgc tgtggggcat tttactttag      1200

gttgcgtatt ggaagatcaa gagcatcaag tcgctaaaga agaaagggaa acacctacta      1260
```

```
ctgatagtat gccgccatta ttacgacaag ctatcgaatt atttgatcac caaggtgcag    1320

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tttatttgtg aaatttgtga tgctattgct ttatttgtaa ccattataag ctgcaataaa    1920

caagttaaca acaacaattg cattcatttt atgtttcagg ttcagggga ggtgtgggag    1980

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acggctacac tagaaggaca gtatttggta tctgcgctct gctgaagcca gttaccttcg    3120

gaaaaagagt tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt    3180

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tctaaagtat atatgagtaa acttggtctg acagttacca atgcttaatc agtgaggcac      3420

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taactacgat acgggagggc ttaccatctg gccccagtgc tgcaatgata ccgcgagacc      3540

cacgctcacc ggctccagat ttatcagcaa taaaccagcc agccggaagg gccgagcgca      3600

gaagtggtcc tgcaacttta tccgcctcca tccagtctat taattgttgc cgggaagcta      3660

gagtaagtag ttcgccagtt aatagtttgc gcaacgttgt tgccattgct acaggcatcg      3720

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